

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Nucleic acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140>

<141>

<150> DE-198 19 829.9

<151> 1998-05-04

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2886

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (372)..(2681)

<400> 1

ggcacgagaa aaagttgtgg tataaacttt tattttagga aaacgcataa aaataataga 60

aaaacgctct tcgggttgta aagaaaataa gaagacaaaa gaaagacatg aaaacgttgc 120

aaacaataaa gcataatactt gccatattga tataaaggga aatcgtgaaa aggcggtgaa 180

aatttcgtaa gattagttgg tattaaggc agccatgca cacagctaaa aaggaaacta 240

aaaaaaccgc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300

aattatatta ttgtatctt gttagagaca gacaacatat ccgctggcaa caaccaacac 360

cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat 410
 Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp

1 5 10

gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458
 Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe

15 20 25

agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac 506
 Ser Ser Ser Ser Thr Arg Thr Ser Ser Asn Gln Arg His Asn

30 35 40 45

cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554
 Gln Gln Leu Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His

50 55 60

agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602
 Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Glu Pro Ala

65 70 75

tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650
 Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln

80 acg cat ctg caa cag cta gac agc agc aac atg ttg tcg cca aag aca 698
Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr
95 100 105

gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca 746
Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro
110 115 120 125

aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga 794
Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg
130 135 140

cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa 842
Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln
145 150 155

cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc 890
Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr
160 165 170

tat agc aca cca gca gca aca acc agc tgt ccg aca gcc acc tac atg 938
Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met
175 180 185

caa tgt cga gcc agc gac aat gag ttc agt att ccg ata tcg aga cat 986
Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His
190 195 200 205

gat aga gta tcc acg gcc aca ttc gcc tgg gtg ttg cat gtg ctg cag 1034

Asp Arg Val Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln

210

215

220

gtg ctg ctc gtg tcg ctg caa cag tgg caa ctt cac gtg caa cag cga 1082
 Val Leu Leu Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg

225

230

235

tcg gtg cta ctg ttc aga agg atc gca gcg agc acc atc gcc ttc att 1130
 Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile

240

245

250

tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc 1178
 Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser

255

260

265

agt agc agc agc aac agc agc aac aac agc agc acg caa ata tta aac 1226
 Ser Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn

270

275

280

285

gga ctt aat aaa cac tca tgg ata ttt tta ttg ata tat ttg aat tta 1274
 Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu

290

295

300

tct gct aaa gtt tgc cta gca gga tat cat gaa aag aga ctg tta cac 1322
 Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His

305

310

315

gat ctt ttg gat cct tat aat aca cta gaa cgt ccc gtt ctc aat gaa 1370
 Asp Leu Leu Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu

320

325

330

tcg gac ccg tta caa tta agc ttt ggt tta act tta atg caa att atc 1418
 Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
 335 340 345

gat gtg gac gag aaa aat caa ttg cta gtc act aat gtg tgg tta aaa 1466
 Asp Val Asp Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys
 350 355 360 365

ctg gag tgg aac gac atg aat ctc cgc tgg aac acc tcc gac tat ggc 1514
 Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Tyr Gly
 370 375 380

gga gtt aag gat ctg cga ata ccg ccg cat cgc atc tgg aag ccg gac 1562
 Gly Val Lys Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp
 385 390 395

gtg ctg atg tac aac agt gcg gat gag gga ttt gac ggc acc tac cag 1610
 Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln
 400 405 410

acg aac gtg gtg gtg cgg aac aac ggc tcg tgt cta tac gtt ccg ccg 1658
 Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro
 415 420 425

ggg atc ttc aag tcg acg tgc aag atc gac atc acg tgg ttc ccc ttc 1706
 Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe
 430 435 440 445

gat gac cag cgg tgc gag atg aag ttc ggc agt tgg acc tac gac gga 1754
 Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly
 450 455 460

ttc cag ctg gat tta caa tta caa gat gaa act ggc ggt gat atc agc 1802
 Phe Gln Leu Asp Leu Gln Leu Gln Asp Glu Thr Gly Gly Asp Ile Ser

465 470 475

agt tac gtg ctc aac ggc gag tgg gaa cta ctg ggt gtg ccc ggc aaa 1850
 Ser Tyr Val Leu Asn Gly Glu Trp Glu Leu Leu Gly Val Pro Gly Lys

480 485 490

cgt aac gag atc tat tac aac tgc tgc ccg gaa ccc tat ata gac atc 1898
 Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile

495 500 505

acc ttc gcc atc atc atc cgc cga cga aca ctg tac tat ttc ttc aac 1946
 Thr Phe Ala Ile Ile Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn

510 515 520 525

ctg atc ata cct tgt gta ctg att gcc tcc atg gcc ttg ctc gga ttc 1994
 Leu Ile Ile Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe

530 535 540

acc ctg ccg cca gat tcg ggt gaa aaa tta tcg ctg ggt gtt acc atc 2042
 Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile

545 550 555

ttg atc tcg ctg acc gtg ttt ctg aat atg gtt gcc gag aca atg ccg 2090
 Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro

560 565 570

gct act tcc gat gcg gtg cca ttg tgg ata cgc atc gtg ttt ttg tgc 2138
 Ala Thr Ser Asp Ala Val Pro Leu Trp Ile Arg Ile Val Phe Leu Cys

575

580

585

tgg ctg cca tgg ata ttg cga atg agt cgc cca gga cga ccg ctg atc 2186

Trp Leu Pro Trp Ile Leu Arg Met Ser Arg Pro Gly Arg Pro Leu Ile

590

595

600

605

cta gag ttc ccg acc acg ccc tgt tcg gac aca tcc tcc gag cgg aag 2234

Leu Glu Phe Pro Thr Thr Pro Cys Ser Asp Thr Ser Ser Glu Arg Lys

610

615

620

cac cag ata ctc tcc gac gtt gag ctg aaa gag cgc tcg tcg aaa tcg 2282

His Gln Ile Leu Ser Asp Val Glu Leu Lys Glu Arg Ser Ser Lys Ser

625

630

635

ctg ctg gcc aac gta cta gac atc gat gat gac ttc cgg cac aat tgt 2330

Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Asn Cys

640

645

650

cgc ccc atg acg ccc ggc gga aca ctg cca cac aac ccg gct ttc tat 2378

Arg Pro Met Thr Pro Gly Gly Thr Leu Pro His Asn Pro Ala Phe Tyr

655

660

665

cgc acg gtt tat gga caa ggc gac gat ggc agc att ggg cca att ggc 2426

Arg Thr Val Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly

670

675

680

685

agc acc cga atg ccg gat gcg gtc acc cat cat acg tgc atc aaa tca 2474

Ser Thr Arg Met Pro Asp Ala Val Thr His His Thr Cys Ile Lys Ser

690

695

700

tca act gaa tat gaa tta ggt tta atc tta aag gaa att cgc ttt ata 2522

Ser Thr Glu Tyr Glu Leu Gly Leu Ile Leu Lys Glu Ile Arg Phe Ile

705

710

715

act gat cag cta cgt aaa gat gac gag tgc aat gac att gcc aat gat 2570

Thr Asp Gln Leu Arg Lys Asp Asp Glu Cys Asn Asp Ile Ala Asn Asp

720

725

730

tgg aaa ttt gca gct atg gtc gtt gac aga ctg tgc ctt atc ata ttc 2618

Trp Lys Phe Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe

735

740

745

aca atg ttc gca ata tta gcc aca ata gct gta cta cta tcg gca cca 2666

Thr Met Phe Ala Ile Leu Ala Thr Ile Ala Val Leu Leu Ser Ala Pro

750

755

760

765

cat att att gtc tcg tagccatatg ggcgagggtgg ttattgttat tggttttatt 2721

His Ile Ile Val Ser

770

ataaaaatcaa tttgttaatt attaaattaa taacgaaact ctttaagtaa attaaaacta 2781

aaaagacact aaaaaagcac aaaaaaatag gaaaatacat gataaaaccc atgaactaaa 2841

taatacatcc aagaaaaacc aaaacaaaaaa aaaaaaaaaa aaaaa 2886

<210> 3
 <211> 3701
 <212> DNA
 <213> *Heliothis virescens*

<220>
 <221> CDS
 <222> (335)..(1822)

<400> 3
 ggcacgagcc gctccccac ggtcgccgc actccgctga acaacaatgc tcaaaaacac 60
 gccgtgactc cacacacatc ccctcgccgc agtaggcgtat gttttagggat cggacggcac 120
 gcgtggccgt cggcgagcgg tcgtgaacaa gttgcataca tatgaaaacc gtaaaaagat 180
 tgaattttaa gccgatcgtt ttcgatagat cctaatacag aagcgggagt gcccgtttg 240
 taggcgggg gtcgagtcgc ggggtcgggg gaaatggcgc ggcgcggggc ggcggcggcgc 300
 gcgccgcgcg gcgccgcgc gtcgcggcgc tgac atg ggc ggg cgg gcg cgc cgc 355
 Met Gly Gly Arg Ala Arg Arg

1

5

tcg cac ttg gcg gcg ccc ggc ctg ctg ctg ctg tgc ctg ctc 403
 Ser His Ile Ala Ala Pro Ala Gly Leu Leu Leu Leu Cys Leu Leu
 10 15 20

tgg ccg agg ggg gca cgc tgc ggg tac cac gag aag cgg cta ctg cac 451
 Tyr Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
 25 30 35

10

cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu

40 45 50 55

agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547
Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gin Ile Ile

60 65 70

gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595
Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys

75 80 85

cta gag tgg aat gat atg aac ttg agg tgg aac act tca gat ttc ggc 643
Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Phe Gly

90 95 100

ggg gtc aaa gat tta aga gtg cca ccc cac aga cta tgg aaa cca gac 691
Gly Val Lys Asp Leu Arg Val Pro Pro His Arg Leu Trp Lys Pro Asp

105 110 115

gtc ctt atg tac aac agc gcg gac gaa ggg ttc gac agc acg tat cca 739
Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Ser Thr Tyr Pro

120 125 130 135

acg aac gtg gtg cgg aac aac ggc tcg tgt ctg tac gtg ccc ccc 787
Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro

140 145 150

ggc atc ttc aag agc acc tgc aag atc gac atc acc tgg ttc ccc ttc 835
Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe

155

160

165

gac gac caa cga tgc gag atg aag ttt ggc agc tgg act tat gat ggt 883
 Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly

170

175

180

tat cag ttg gat cta caa cta cag gat gaa ggg ggc gga gat ata agc 931
 Tyr Gln Leu Asp Leu Gln Leu Gln Asp Glu Gly Gly Asp Ile Ser

185

190

195

agt ttt gtc acg aat ggc gaa tgg gag tta ata gga gtc ccc ggc aag 979
 Ser Phe Val Thr Asn Gly Glu Trp Glu Leu Ile Gly Val Pro Gly Lys

200

205

210

215

cgc aac gag atc tac tac aac tgt tgt ccg gag cca tac atc gac atc 1027
 Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile

220

225

230

acg ttt gcg gtg gtg atc cgg agg aaa acg ctc tac tac ttc ttc aat 1075
 Thr Phe Ala Val Val Ile Arg Arg Lys Thr Leu Tyr Tyr Phe Phe Asn

235

240

245

ctg atc gtg ccc tgc gtg ctc atc gcc tcc atg gct cta ttg ggg ttc 1123
 Leu Ile Val Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe

250

255

260

acc ttg cct cca gac tcc gga gaa aag ttg tct tta ggt gtg acg ata 1171
 Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile

265

270

275

tta ctg tcg ttg acg gtg ttc ctc aac atg gtg gcg gag acg atg cca 1219

Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro

280

285

290

295

gcg acg tcg gac gcc gtg ccc ttg ctc ggc acc tac ttc aac tgc atc 1267

Ala Thr Ser Asp Ala Val Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile

300

305

310

atg ttc atg gtg gct tcc tcc gtc gtc tcc acc ata ctg atc ctc aac 1315

Met Phe Met Val Ala Ser Ser Val Val Ser Thr Ile Leu Ile Leu Asn

315

320

325

tac cac cac cgg cac gca gac act cac gaa atg agt gat tgg att cgt 1363

Tyr His His Arg His Ala Asp Thr His Glu Met Ser Asp Trp Ile Arg

330

335

340

tgc gtg ttc ctt tat tgg ctg ccg tgg gtg ctg cgc atg tca cgg ccc 1411

Cys Val Phe Leu Tyr Trp Leu Pro Trp Val Leu Arg Met Ser Arg Pro

345

350

355

ggc tcg gcg acg acg cgg ccg ccg gcg cgc gta cct ccg ccg ccg gac 1459

Gly Ser Ala Thr Thr Pro Pro Pro Ala Arg Val Pro Pro Pro Pro Asp

360

365

370

375

ctg gag ctg cgc gag cgc tcc tcc aag tcg ctc cta gcg aac gtg ctc 1507

Leu Glu Leu Arg Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu

380

385

390

gac atc gat gac gac ttc cgc cac ccg caa gcg cag cag ccg caa tgc 1555

Asp Ile Asp Asp Asp Phe Arg His Pro Gln Ala Gln Gln Pro Gln Cys

395

400

405

tgc cga tac tac agg ggg ggt gag gag aat ggc gcg ggg ttg gcg gcg 1603
 Cys Arg Tyr Tyr Arg Gly Gly Glu Glu Asn Gly Ala Gly Leu Ala Ala
 410 415 420

cac agt tgc ttc ggt gtc gac tac gag ctc tcc ctc att ctg aag gag 1651
 His Ser Cys Phe Gly Val Asp Tyr Glu Leu Ser Leu Ile Leu Lys Glu
 425 430 435

att aga gtc atc aca gat cag atg cgc aag gac gac gaa gat gcg gac 1699
 Ile Arg Val Ile Thr Asp Gln Met Arg Lys Asp Asp Glu Asp Ala Asp
 440 445 450 455

att tcg cgc gac tgg aag ttc gcc gcc atg gtc gtg gac aga ctg tgc 1747
 Ile Ser Arg Asp Trp Lys Phe Ala Ala Met Val Val Asp Arg Leu Cys
 460 465 470

ctt att atc ttt acc ctg ttc aca atc atc gcc acg cta gcc gtg ctg 1795
 Leu Ile Ile Phe Thr Leu Phe Thr Ile Ile Ala Thr Leu Ala Val Leu
 475 480 485

ctg tcc gcg cca cac atc atg gtg tcg tagcgacccg cccgcttgcg 1842
 Leu Ser Ala Pro His Ile Met Val Ser
 490 495

gatacgcatg cgaaaagttc tgtgataccg cgaatatttg ttaagttgtg atgagcgaag 1902

tggcgccgac ggtgacgcccg cggcgctcgga gttgcccggc cctgcctcgc cgcggcgcc 1962

cccctgtaga cataagttac cgctgactgc caaccctgta cgttcaacaa ataactgccc 2022

atccgactaa cgtctttat ccccttgaaa aattcagcga ttgtgtaccc ctttcttcca 2082

agaatacaat gacaaatggt cgtcacgctc agtggaatca atcccgtact cttcgcccga 2142

tatccctt aggtatgtc acgagttga atgagcggtt ccgtatcaga cgttccgtc 2202

ccggaacggt cgtccctgc gataaagtgg cagtagtgc tatacaggca cttaaggccg 2262

ccacgcccacg ggcgcgcggc ggcgtcgccc cggaaacccg cgaccctcac cgctgcaagt 2322

ggccacccac tagacaagac tgccgcagaa aatatttgc aaaaaacgtc ttcccttctta 2382

ccgatgaacg acctgattcg cattaaaat taaactttgt tagaacttct tcgattctt 2442

aaatctattt tacagtttag agtttggcg gtgaaacaat ggccctttgt ttcccttctt 2502

ttcgattcca tgaatcgtgg ttataatccc tagtttatt ttccggatata tttgtgtcag 2562

tagctagtat agaactttac aaacaatgtt gattcaattt gtacaggtt tgatatgcct 2622

cgttgtgaac gggccgata ttgttataaa tggtaaaata cccatggcta tagcttaata 2682

aatcgttcgt taaaagttgt agttaaacaat atatttttt aataaagtca tatctgggtc 2742

ttccggaaacg acttttacaa ataattaaat tacatattaa tatcacgtt gtacttctt 2802

ccatacagtt acagtaattt gtagtgcgaa aataatatta gcttggtaaaa ttcccttctt 2862

cggaaatttt ttcacacaga tgccgaccatc gtttcaaca tttacatgtt atatagaact 2922

cattttataa gatatacaac attttataag tacaagaatgtt tgtaacatgtt accgggtttt 2982

cgttacatag agggtataac acaaagggtgc ctacatattg acagatgcga agcacgatca 3042

gttgataagc acaggtacac tatacctga catccgacag tcctgccgt cgtctgccac 3102

actcgaaac attcgacagt tcagttact gctccgcat catcgattgt taagttgtt 3162

gttctaactc atcgcatca tttcattcaa aaacattgt aaccttcaa gggaaaacg 3222

tgttgtaaac agtgagagtgcgcgggtaca accgacacgc gaatgtaccc tcgcaaggct 3282

cctgtaatgt tttccttgc cgaggtgttgc tgagagtaa tcttagacgg tccgatggaa 3342

gttgcggacc ggtatgtt acaagtcaat gtttttaagt catccgttta tttattgtt 3402

tatcttctta ccattcgcta gaggttgtgt gacgaccgg acggggcgccgcaacccg 3462

cacacgcggg gttccatctt tgtatttagat ggaagttgtgcggcatctt ccgtcgaa 3522

tgggacaacc cgttgcggcc aacattttttttaattgttag gtttaactctt gaattgcact 3582

ttgtttatataatataaaacg aatgaaacaa aaaaaaaaaaaa aaaaaactcg agagtacttc 3642

tagagcggcc gcgggccccat cgattttcca cccgggtggg gtaccargta agtgtaccc 3701

<210> 5
<211> 3109
<212> DNA
<213> *Heliothis virescens*

<220>
<221> CDS
<222> (95)..(1597)

<400> 5

ggcacgagcc ggccgcacgt tgtcccaggc cgcatgagcg cgccggcgtg ctagcgcagc 60

gtgcgcgggt gtggtatgcc cgcgcgtcgc cgat atg gcc cct atg ttg gcg gcc 115
Met Ala Pro Met Leu Ala Ala

1

5

ttg gcg ctg ctg gct ttg ctg ccc gta tcg gag caa ggt cct cac gag 163
Leu Ala Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu

10

15

20

aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211
Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg

25

30

35

ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259
Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr

40

45

50

55

ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307

Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr

60

65

70

aat ata tgg ctg tcg ttg gag tgg aat gac tac aac ctg agg tgg aac

355

Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn

75

80

85

gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag

403

Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys

90

95

100

ttg tgg aag ccg gac gtc ctt atg tat aat aat gct gac gag ggt ttt

451

Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe

105

110

115

gac ggg acc tac cag acc aac gtg gtg gtc aga agc ggc ggc agt tgc

499

Asp Gly Thr Tyr Gln Thr Asn Val Val Val Arg Ser Gly Gly Ser Cys

120

125

130

135

ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc

547

Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile

140

145

150

gcg tgg ttc ccc ttc gac gac caa cac tgt gat atg aag ttc ggt agc

595

Ala Trp Phe Pro Phe Asp Asp Gln His Cys Asp Met Lys Phe Gly Ser

155

160

165

tgg aca tat gac ggc aat cag ttg gat ctg gtg cta aaa gat gag gca

643

Trp Thr Tyr Asp Gly Asn Gln Leu Asp Leu Val Leu Lys Asp Glu Ala

170

175

180

ggc ggc gat cta tcg gac ttc ata aca aat ggg gag tgg tat cta ata 691
 Gly Gly Asp Leu Ser Asp Phe Ile Thr Asn Gly Glu Trp Tyr Leu Ile
 185 190 195

gga atg cca ggc aaa aag aac aca ata aca tac gcg tgc tgc ccc gag 739
 Gly Met Pro Gly Lys Lys Asn Thr Ile Thr Tyr Ala Cys Cys Pro Glu
 200 205 210 215

ccc tac gtg gac gtc acc ttc acc atc atg ata aga aga cga acc ttg 787
 Pro Tyr Val Asp Val Thr Phe Thr Ile Met Ile Arg Arg Arg Thr Leu
 220 225 230

tac tac ttc ttc aac ctg atc gtc ccc tgc gtg ctg atc tca tcg atg 835
 Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ser Ser Met
 235 240 245

gca ctc ctc ggc ttc aca ctg cca cca gac tcc gga gag aaa ctc aca 883
 Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Thr
 250 255 260

ctt gga gtc act att ctt cta tcg ctg acg gtg ttc ctc aac ctg gta 931
 Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn Leu Val
 265 270 275

gcc gag acc ctg cca cag gtc tcc gac gct atc ccc ctg tta ggg acg 979
 Ala Glu Thr Leu Pro Gln Val Ser Asp Ala Ile Pro Leu Leu Gly Thr
 280 285 290 295

tac ttc aat tgc atc atg ttc atg gta gcg tcg tct gtg gta ctg act 1027
 Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val Leu Thr
 300 305 310

gtg gtg gta ctc aat tac cac cat cga aca gct gat ata cat gaa atg 1075
 Val Val Val Leu Asn Tyr His His Arg Thr Ala Asp Ile His Glu Met

315 320 325

cca cag tgg ata aaa tca gta ttc cta caa tgg ttg cca tgg ata ctg 1123
 Pro Gln Trp Ile Lys Ser Val Phe Leu Gln Trp Leu Pro Trp Ile Leu

330 335 340

cga atg tcg agg cca ggg aag aag atc acc agg aag act ata atg atg 1171
 Arg Met Ser Arg Pro Gly Lys Lys Ile Thr Arg Lys Thr Ile Met Met

345 350 355

aac acg agg atg agg gag ctg gaa ctg aag gag agg tcg tcg aag tcc 1219
 Asn Thr Arg Met Arg Glu Leu Glu Leu Lys Glu Arg Ser Ser Lys Ser
 360 365 370 375

ttg ctg gcg aat gtt cta gat att gat gat gac ttc aga cac ggc cct 1267
 Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Gly Pro
 380 385 390

ccg cct cct aac agt act gcc tcg acc ggg aat ttg gga cct ggg tgc 1315
 Pro Pro Pro Asn Ser Thr Ala Ser Thr Gly Asn Leu Gly Pro Gly Cys
 395 400 405

tca ata ttc cgc acg gat ttc cgt cgg tcg ttc gtc cgt ccg tcc acg 1363
 Ser Ile Phe Arg Thr Asp Phe Arg Arg Ser Phe Val Arg Pro Ser Thr
 410 415 420

atg gaa gac gtg ggc ggc ggg ctg ggt agc cac cat cgc gag ctg cac 1411
 Met Glu Asp Val Gly Gly Leu Gly Ser His His Arg Glu Leu His

425

430

435

ctc ata ctg aga gag ctg cag ttc atc acg gcc agg atg aag aag gct 1459

Leu Ile Leu Arg Glu Leu Gln Phe Ile Thr Ala Arg Met Lys Lys Ala

440

445

450

455

gat gag gaa gcc gag ctg atc agc gac tgg aag ttt gct gcg atg gtt 1507

Asp Glu Glu Ala Glu Leu Ile Ser Asp Trp Lys Phe Ala Ala Met Val

460

465

470

gtt gat agg ttt tgc ctg ttc gtg ttc aca ctt ttc aca atc atc gcg 1555

Val Asp Arg Phe Cys Leu Phe Val Phe Thr Leu Phe Thr Ile Ile Ala

475

480

485

aca gta gct gtc ctg tta tcg gca ccg cat atc atc gtg caa 1597

Thr Val Ala Val Leu Leu Ser Ala Pro His Ile Ile Val Gln

490

495

500

tgaaccaacc actgagccgg caactccggc gcatgaatga gagaataat tattagatcg 1657

ccgatttgta attataattg ataatgtaat taaattaaat acgtgggtga aacgcacacg 1717

tctccataac aaagtttaa gacattaaat tatgataaaat ttacatattg tagttaagtc 1777

gagtgttcat gaaatttta gccggcgcaa ggagttcgt gaaggctgt atatatttt 1837

tcttattgtt gtatattgta tcgttgttca tgtttcttt caggaagtga gctttgtact 1897

gtttgttct tcgatggcag gtgcacttca gttcaggctg aaatttccat taacattat 1957

ttaaacaat gtgatgttga ctaggatgtt atacagataa atgttgacgt gtataattt 2017

ttaaaataaa caatattaat tactattact aaacgatatt ataaacgaag tactaacgag 2077

ggttacttta atgggaagaa cgctaagctg gcacagagtt gcattaattt gaaaaaagaa 2137

attacggaaa aaagtttatt gaaaattgaa cttttggaa ggaaagtaac gtttgatcaa 2197

aaaagtttgtt aaaacgaaag ttcggttctg cgccaaatact ggaattaaaa ttctcgtaaa 2257

tattaggaa aagaaggcctt ttaaaacaa aagatttcaa ccggcatoct ttttacaagt 2317

aatgagggat cacagatgtat gacaaaaaaac cttagggatataagtaatg tacataatgg 2377

atcaaatac ggttagagtca agaatagttt acgatttaag attattccat tcgatattaa 2437

aattcgatta gcgattgtcg ctgcgtctac tttgatacat atcgatttga atcgatattg 2497

tataaattta gatagatcgacat tagtataa tgagtatgaa cgtttaattt tttaaaaaaag 2557

aatgtactac gaagatttttccaggaattt gttaaacagt tatggatttga ataaagaaatc 2617

aacaattaat acggaaccaa aggttagacta ggtgtacat caggagatttga aatttttaca 2677

taaatttaggaccgacttaaa tggaaacttgc gagtgatttga ataaactttt aattttaaaa 2737

ctcattgtcg attaaatggaa gaataactttt tgatctctcg tatcgataaa tgctcactta 2797

actatcgata gcgtatattt ataaactgttta gtatatcgat atgggatgaa gtcactagca 2857

tcagaaatag tcattaatggaa ggaatcggtt tgggttaatg ttatgcttag cgaaaatattt 2917

acaatgctgt tgatatcact aaccatcacy taaccatatt gataaaatgt aaatacagaa ~~2977~~

tattgcgtg tgtatttta tataaatttt agaaaaaaaaaaa aaaaaaaaaa aactcgagag 3037

tacttctaga gcggccgcgg gccccatcgat tttccacccg ggtgggtac caggtaagtg 3097

tacccaaattc gc

3109